

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER

0 (ii) TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES

5 (iii) NUMBER OF SEQUENCES: 19

0 (iv) CORRESPONDENCE ADDRESS:
5 (A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071

0 (v) COMPUTER READABLE FORM:
5 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1

0 (vi) CURRENT APPLICATION DATA:
5 (A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE:
(C) CLASSIFICATION:

0 (vii) PRIOR APPLICATION DATA:
Prior applications total,
including application
described below: 1

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Guise, Jeffrey W.
(B) REGISTRATION NUMBER: 34,613
(C) REFERENCE/DOCKET NUMBER: 212/127

(ix) TELECOMMUNICATION INFORMATION:

10 (A) TELEPHONE: (619) 552-8400
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(C) TELEX: 67-3510

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SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 3517 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

15 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 124...2445

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCCGGGGTT ACAGGCTGGC CAGCAGGCTG TGCAGGCGAG TCCGGTCAGCAGGAGGGAA	60
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GAAGTGGCCT AAAATCTCTC CCGCATCGGC AGCCCAGGCC TAGTGCCCTA CCAGCCACCA	120
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25 GCC ATG GCT CTC TTC TTG CTC ACC TGC CTG CTG GCT GTC TTT TCA GCG Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala	168
1 5 10 15	

30 GCC ACG GCA CAA AGC TCC TTA TTG GGT CCC AGC TCC ATA TTT GGT CCC Ala Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro	216
20 25 30	

35 GGG GAG GTG AAT GTT TTG GAA GGC GAC TCG GTG TCC ATC ACA TGC TAC Gly Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr	264
35 40 45	

40 TAC CCA ACA ACC TCC GTC ACC CGG CAC AGC CGG AAG TTC TGG TGC CGG Tyr Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg	312
50 55 60	

45 GAA GAG GAG AGC GGC CGC TGC GTG ACG CTT GCC TCG ACC GGC TAC ACG Glu Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr	360
65 70 75	

50 TCC CAG GAA TAC TCC GGG AGA GGC AAG CTC ACC GAC TTC CCT GAT AAA Ser Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys	408
80 85 90 95	

55 GGG GAG TTT GTG GTG ACT GTT GAC CAA CTC ACC CAG AAC GAC TCA GGG Gly Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly	456
100 105 110	

60 AGC TAC AAG TGT GGC GTG GGA GTC AAC GGC CGT GGC CTG GAC TTC GGT Ser Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly	504
115 120 125	

65 GTC AAC GTG CTG GTC AGC CAG AAG CCA GAG CCT GAT GAC GTT GTT TAC Val Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr	552
130 135 140	

70 AAA CAA TAT GAG AGT TAT ACA GTA ACC ATC ACC TGC CCT TTC ACA TAT Lys Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr	600
145 150 155	

75 GCG ACT AGG CAA CTA AAG AAG TCC TTT TAC AAG GTG GAA GAC GGG GAA	648

	Ala Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu	160 165 170 175	
5	CTT GTA CTC ATC ATT GAT TCC AGC AGT AAG GAG GCA AAG GAC CCC AGG Leu Val Leu Ile Ile Asp Ser Ser Ser Lys Glu Ala Lys Asp Pro Arg	180 185 190	696
10	TAT AAG GGC AGA ATA ACG TTG CAG ATC CAA AGT ACC ACA GCA AAA GAA Tyr Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu	195 200 205	744
15	TTC ACA GTC ACC ATC AAG CAT TTG CAG CTC AAT GAT GCT GGG CAG TAT Phe Thr Val Thr Ile Lys His Leu Gln Leu Asn Asp Ala Gly Gln Tyr	210 215 220	792
20	GTC TGC CAG AGT GGA AGC GAC CCC ACT GCT GAA GAA CAG AAC GTT GAC Val Cys Gln Ser Gly Ser Asp Pro Thr Ala Glu Glu Gln Asn Val Asp	225 230 235	840
25	CTC CGA CTG CTA ACT CCT GGT CTG CTC TAT GGA AAC CTG GGG GGC TCG Leu Arg Leu Leu Thr Pro Gly Leu Leu Tyr Gly Asn Leu Gly Gly Ser	240 245 250 255	888
30	GTG ACC TTT GAA TGT GCC CTG GAC TCT GAA GAC GCA AAC GCG GTA GCA Val Thr Phe Glu Cys Ala Leu Asp Ser Glu Asp Ala Asn Ala Val Ala	260 265 270	936
35	TCC TTG CGC CAG GTT AGG GGT GGC AAT GTG GTC ATT GAC AGC CAG GGG Ser Leu Arg Gln Val Arg Gly Gly Asn Val Val Ile Asp Ser Gln Gly	275 280 285	984
40	ACA ATA GAT CCA GCC TTC GAG GGC AGG ATC CTG TTC ACC AAG GCT GAG Thr Ile Asp Pro Ala Phe Glu Gly Arg Ile Leu Phe Thr Lys Ala Glu	290 295 300	1032
45	AAC GGC CAC TTC AGT GTA GTG ATC GCA GGC CTG AGG AAG GAA GAC ACA Asn Gly His Phe Ser Val Val Ile Ala Gly Leu Arg Lys Glu Asp Thr	305 310 315	1080
50	CCC ACC CAG CTT CGG CAA CTC TTC GTC AAT GAA GAG ATC GAC GTG TCC Pro Thr Gln Leu Arg Gln Leu Phe Val Asn Glu Glu Ile Asp Val Ser	340 345 350	1128
55	CGC AGC CCC CCT GTG TTG AAG GGC TTT CCA GGA GGC TCC GTG ACC ATA Arg Ser Pro Pro Val Leu Lys Gly Phe Pro Gly Gly Ser Val Thr Ile	355 360 365	1176
60	CGC TGC CCC TAC AAC CCG AAG AGA AGC GAC AGC CAC CTG CAG CTG TAT Arg Cys Pro Tyr Asn Pro Lys Arg Ser Asp Ser His Leu Gln Leu Tyr	370 375 380	1224
65	CTC TGG GAA GGG AGT CAA ACC CGC CAT CTG CTG GTG GAC AGC GGC GAG Leu Trp Glu Gly Ser Gln Thr Arg His Leu Leu Val Asp Ser Gly Glu	385 390 395	1272
	GGG CTG GTT CAG AAA GAC TAC ACA GGC AGG CTG GCC CTG TTC GAA GAG Gly Leu Val Gln Lys Asp Tyr Thr Gly Arg Leu Ala Leu Phe Glu Glu	400 405 410 415	1320
	CCT GGC AAT GGC ACC TTC TCA GTC GTC CTC AAC CAG CTC ACT GCC GAG Pro Gly Asn Gly Thr Phe Ser Val Val Leu Asn Gln Leu Thr Ala Glu	420 425 430	1368
			1416

	GAT GAA GGC TTC TAC TGG TGT GTC AGC GAT GAC GAT GAG TCC CTG ACG Asp Glu Gly Phe Tyr Trp Cys Val Ser Asp Asp Asp Glu Ser Leu Thr 435 440 445	1464
5	ACT TCG GTG AAG CTC CAG ATC GTT GAC GGA GAA CCA AGC CCC ACG ATC Thr Ser Val Lys Leu Gln Ile Val Asp Gly Glu Pro Ser Pro Thr Ile 450 455 460	1512
10	GAC AAG TTC ACT GCT GTG CAG GGA GAG CCT GTT GAG ATC ACC TGC CAC Asp Lys Phe Thr Ala Val Gln Gly Glu Pro Val Ile Thr Cys His 465 470 475	1560
15	TTC CCA TGC AAA TAC TTC TCC TCC GAG AAG TAC TGG TGC AAG TGG AAT Phe Pro Cys Lys Tyr Phe Ser Ser Glu Tyr Trp Cys Lys Trp Asn 480 485 490 495	1608
20	GAC CAT GGC TGC GAG GAC CTG CCC ACT AAG CTC AGC TCC AGC GGC GAC Asp His Gly Cys Glu Asp Leu Pro Thr Lys Leu Ser Ser Gly Asp 500 505 510	1656
25	CTT GTG AAA TGC AAC AAC CTG GTG CTC ACC CTG ACC TTG GAC TCG Leu Val Lys Cys Asn Asn Asn Leu Val Leu Thr Leu Thr Leu Asp Ser 515 520 525	1704
30	GTC AGC GAA GAT GAC GAG GGC TGG TAC TGG TGT GGC GCG AAA GAC GGG Val Ser Glu Asp Asp Glu Gly Trp Tyr Trp Cys Gly Ala Lys Asp Gly 530 535 540	1752
35	CAC GAG TTT GAA GAG GTT GCG GCC GTC AGG GTG GAG CTG ACA GAG CCA His Glu Phe Glu Glu Val Ala Ala Val Arg Val Glu Leu Thr Glu Pro 545 550 555	1800
40	GCC AAG GTA GCT GTC GAG CCA GCC AAG GTA CCT GTC GAC CCA GCC AAG Ala Lys Val Ala Val Glu Pro Ala Lys Val Pro Val Asp Pro Ala Lys 560 565 570 575	1848
45	GCA GCC CCC GCG CCT GCT GAG GAG AAG GCC AAG GCG CGG TGC CCA GTG Ala Ala Pro Ala Pro Ala Glu Glu Lys Ala Lys Ala Arg Cys Pro Val 580 585 590	1896
50	CCC AGG AGA AGG CAG TGG TAC CCA TTG TCA AGG AAG CTG AGA ACA AGT Pro Arg Arg Arg Gln Trp Tyr Pro Leu Ser Arg Lys Leu Arg Thr Ser 595 600 605	1944
55	TGT CCA GAA CCT CGG CTC CTT GCG GAG GAG GTA GCA GTG CAG AGT GCG Cys Pro Glu Pro Arg Leu Leu Ala Glu Val Ala Val Gln Ser Ala 610 615 620	1992
60	GAA GAC CCA GCC AGT GGG AGC AGA GCG TCT GTG GAT GCC AGC AGT GCT Glu Asp Pro Ala Ser Gly Ser Arg Ala Ser Val Asp Ala Ser Ser Ala 625 630 635	2040
65	TCG GGA CAA AGC GGG AGT GCC AAA GTA CTG ATC TCC ACC CTG GTG CCC Ser Gly Gln Ser Gly Ser Ala Lys Val Leu Ile Ser Thr Leu Val Pro 640 645 650 655	2088
70	TTG GGG CTG GTG CTG GCA GCG GGG GCC ATG GCC GTG GCC ATA GCC AGA Leu Gly Leu Val Leu Ala Ala Gly Ala Met Ala Val Ala Ile Ala Arg 660 665 670	2136
75	GCC CGG CAC AGG AGG AAC GTG GAC CGA GTT TCC ATC GGA AGC TAC AGG Ala Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg 675 680 685	2184
80	ACA GAC ATT AGC ATG TCA GAC TTG GAG AAC TCC AGG GAG TTC GGA GCC Thr Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala	2232

	690	695	700	
5	ATT GAC AAC CCA AGC GCC TGC CCC GAT GCC CGG GAG ACG GCC CTC GGA Ile Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly 705 710 715			2280
10	GGA AAG GAT GAG TTA GCG ACG GCC ACC GAG AGC ACC GTG GAG ATT GAG Gly Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu 720 725 730 735			2328
15	GAG CCC AAG AAG GCA AAA CGG TCA TCC AAG GAA GAA GCC GAC CTG GCC Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala 740 745 750			2376
20	TAC TCA GCT TTC CTG CTC CAA TCC AAC ACC ATA GCT GCT GAG CAC CAA Tyr Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln 755 760 765			2424
25	GAT GGC CCC AAG GAG GCC TAG GCACAGCCGG CCACCGCCGC CGCCGCCACC GCCGC Asp Gly Pro Lys Glu Ala 770			2480
30	CGCCGCCGCC ACCTGTGAAA ATCACCTTCC AGAACATCACGT TGATCCTCGG GGTCCCCAGA GCCGGGGCT CAACCGCCCT GCACCCCCCA TGTCCTCACC ACCTAAACTT CCCTACCTGT GCCAGAGGT GTGCTGGTCC CCTCCTCCAC GGCACTCCAGG CCTGGCTCAA TGTTCCCGTT GGGGTGGGGG TGTGAGGGGT TCCTACTTGC AGCCCGGTTC TCCCAGAGAGA AGCTAAGGAT CCAGGTCTG AGGGAGGGGC CTCTCGAAGG CAGACAGACC AGAGAGGGGG GAGGAGCCCT TGGATGGGAG GCCAGAGGCG CTTCCGGCC ACCCCCTCCC TCCCTGCCCT CACCCCTCCTT 35		2540	
35	CCTTCATTCA AAAGTCCAG TGGCTGCTGC CTAGGGTCCA GGCGCTGGCC GCACGCCCTCC TCGAAGCCGT TGTGCAAACA TCACTGGAGG AAGCCAGGGC TCCTCCGGG CTGTGTATCC 40		2600	
40	TCACTCAGGC ATCCTGTCTT CCCCAGTATC AGGAGATGTC AAGCGTCTGA AGGCTGTGTG CCCTGGCGT GTCTGCAAGT CACCCAGAC ACATGTTCTC GCCATTTAC AGATGAGAAC ACTGAGGTTG TACTCAAGGG CACCTGCGA GATGGAGCAA CAGCAAACTA GATGGGCTTC 45		2660	
45	TGCTGTCTC TTGGCCAGAG GTCTCTCCAC AGGAGCCCT GCCCTGTAG GAAGCAGAGT TTTAGAACAT GGAAGAAGAA GAGGGGGATG GCCCTGGACG CTGACCTCTC CCAAGCCCCC 50		2720	
50	ACGGGGAAA AGGCCCTCTC CTTTCTGTC ACTCTCGGGG ACCTGCGGAG TTGAGCATTC GTGCCCCGTG TGTCTGAAGA GTTCCCAGTG GAAAGAAGAA AAGAGGGTGT TTGTCAGTGC CGGGGAGGGC CTGATCCCCA GACAGCTGAA GTTTAAGTC CTTGTCCCTG TGAGCTTTAA 55		2780	
55	CCAGCACCTC CGGGCTGACC CTTGCTAACCA CATCAGAAAT GTGATTAAAT CATAAACAT TGTGATTGCC ACTGGGA		2840	
60				3140
65	(2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 773 amino acids			3200
				3260
				3320
				3380
				3440
				3500
				3517

(B) TYPE: amino acid
 (C) STRANNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

	Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala Ala			
	1	5	10	15
10	Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro Gly			
	20	25	30	
15	Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr			
	35	40	45	
	Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg Glu			
	50	55	60	
20	Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr Ser			
	65	70	75	80
	Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys Gly			
	85	90	95	
25	Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly Ser			
	100	105	110	
30	Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly Val			
	115	120	125	
	Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr Lys			
	130	135	140	
35	Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr Ala			
	145	150	155	160
	Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu Leu			
	165	170	175	
40	Val Leu Ile Ile Asp Ser Ser Ser Lys Glu Ala Lys Asp Pro Arg Tyr			
	180	185	190	
45	Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu Phe			
	195	200	205	
	Thr Val Thr Ile Lys His Leu Gln Leu Asn Asp Ala Gly Gln Tyr Val			
	210	215	220	
50	Cys Gln Ser Gly Ser Asp Pro Thr Ala Glu Glu Gln Asn Val Asp Leu			
	225	230	235	240
	Arg Leu Leu Thr Pro Gly Leu Leu Tyr Gly Asn Leu Gly Gly Ser Val			
	245	250	255	
55	Thr Phe Glu Cys Ala Leu Asp Ser Glu Asp Ala Asn Ala Val Ala Ser			
	260	265	270	
60	Leu Arg Gln Val Arg Gly Asn Val Val Ile Asp Ser Gln Gly Thr			
	275	280	285	
	Ile Asp Pro Ala Phe Glu Gly Arg Ile Leu Phe Thr Lys Ala Glu Asn			
	290	295	300	
65	Gly His Phe Ser Val Val Ile Ala Gly Leu Arg Lys Glu Asp Thr Gly			
	305	310	315	320

Asn Tyr Leu Cys Gly Val Gln Ser Asn Gly Gln Ser Gly Asp Gly Pro
 325 330 335

5 Thr Gln Leu Arg Gln Leu Phe Val Asn Glu Glu Ile Asp Val Ser Arg
 340 345 350

Ser Pro Pro Val Leu Lys Gly Phe Pro Gly Gly Ser Val Thr Ile Arg
 355 360 365

10 Cys Pro Tyr Asn Pro Lys Arg Ser Asp Ser His Leu Gln Leu Tyr Leu
 370 375 380

Trp Glu Gly Ser Gln Thr Arg His Leu Leu Val Asp Ser Gly Glu Gly
 385 390 395 400

15 Leu Val Gln Lys Asp Tyr Thr Gly Arg Leu Ala Leu Phe Glu Glu Pro
 405 410 415

Gly Asn Gly Thr Phe Ser Val Val Leu Asn Gln Leu Thr Ala Glu Asp
 20 420 425 430

Glu Gly Phe Tyr Trp Cys Val Ser Asp Asp Asp Glu Ser Leu Thr Thr
 435 440 445

25 Ser Val Lys Leu Gln Ile Val Asp Gly Glu Pro Ser Pro Thr Ile Asp
 450 455 460

Lys Phe Thr Ala Val Gln Gly Glu Pro Val Glu Ile Thr Cys His Phe
 465 470 475 480

30 Pro Cys Lys Tyr Phe Ser Ser Glu Lys Tyr Trp Cys Lys Trp Asn Asp
 485 490 495

His Gly Cys Glu Asp Leu Pro Thr Lys Leu Ser Ser Ser Gly Asp Leu
 35 500 505 510

Val Lys Cys Asn Asn Leu Val Leu Thr Leu Thr Leu Asp Ser Val
 515 520 525

40 Ser Glu Asp Asp Glu Gly Trp Tyr Trp Cys Gly Ala Lys Asp Gly His
 530 535 540

Glu Phe Glu Glu Val Ala Ala Val Arg Val Glu Leu Thr Glu Pro Ala
 545 550 555 560

45 Lys Val Ala Val Glu Pro Ala Lys Val Pro Val Asp Pro Ala Lys Ala
 565 570 575

Ala Pro Ala Pro Ala Glu Glu Lys Ala Lys Ala Arg Cys Pro Val Pro
 50 580 585 590

Arg Arg Arg Gln Trp Tyr Pro Leu Ser Arg Lys Leu Arg Thr Ser Cys
 595 600 605

55 Pro Glu Pro Arg Leu Leu Ala Glu Glu Val Ala Val Gln Ser Ala Glu
 610 615 620

Asp Pro Ala Ser Gly Ser Arg Ala Ser Val Asp Ala Ser Ser Ala Ser
 625 630 635 640

60 Gly Gln Ser Gly Ser Ala Lys Val Leu Ile Ser Thr Leu Val Pro Leu
 645 650 655

65 Gly Leu Val Leu Ala Ala Gly Ala Met Ala Val Ala Ile Ala Arg Ala
 660 665 670

Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg Thr
 675 680 685
 5 Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala Ile
 690 695 700
 Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly Gly
 705 710 715 720
 10 Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu Glu
 725 730 735
 Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala Tyr
 740 745 750
 15 Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln Asp
 755 760 765
 20 Gly Pro Lys Glu Ala
 770

25 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2919 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Human polyimmunoglobulin Receptor

35 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 235....2472

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AGAGTTTCAG TTTGGCAGC AGCGTCCAGT GCCCTGCCAG TAGCTCCTAG AGAGGCAGGG	60
GTTACCAACT GGCCAGCAGG CTGTGTCCCT GAAGTCAGAT CAACGGGAGA GAAGGAAGTG	120
45 GCTAAACAT TGCACAGGAG AAGTCGGCCT GAGTGGTGCG GCGCTCGGGA CCCACCAGCA	180
ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACG AAG	237
50 Lys 1	
AGT CCC ATA TTT GGT CCC GAG GAG GTG AAT AGT GTG GAA GGT AAC TCA	285
Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn Ser	
5 10 15	
55 GTG TCC ATC ACG TGC TAC TAC CCA CCC ACC TCT GTC AAC CGG CAC ACC	333
Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr	
20 25 30	
60 CGG AAG TAC TGG TGC CGG CAG GGA GCT AGA GGT GGC TGC ATA ACC CTC	381
Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr Leu	
35 40 45	
65 ATC TCC TCG GAG GGC TAC GTC TCC AGC AAA TAT GCA GGC AGG GCT AAC	429
Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala Asn	
50 55 60 65	

	CTC ACC AAC TTC CCC GAG AAC GGC ACA TTT GTG GTG AAC ATT GCC CAG Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala Gln 70 75 80	477
5	CTG AGC CAG GAT GAC TCC GGG CGC TAC AAG TGT GGC CTG GGC ATC AAT Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Asn 85 90 95	525
10	AGC CGA GGC CTG TCC TTT GAT GTC AGC CTG GAG GTC AGC CAG GGT CCT Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly Pro 100 105 110	573
15	GGG CTC CTA AAT GAC ACT AAA GTC TAC ACA GTG GAC CTG GGC AGA ACG Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg Thr 115 120 125	621
20	GTG ACC ATC AAC TGC CCT TTC AAG ACT GAG AAT GCT CAA AAG AGG AAG Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg Lys 130 135 140 145	669
25	TCC TTG TAC AAG CAG ATA GGC CTG TAC CCT GTG CTG GTC ATC GAC TCC Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp Ser 150 155 160	717
30	AGT GGT TAT GTG AAT CCC AAC TAT ACA GGA AGA ATA CGC CTT GAT ATT Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp Ile 165 170 175	765
35	CAG GGT ACT GGC CAG TTA CTG TTC AGC GTT GTC ATC AAC CAA CTC AGG Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu Arg 180 185 190	813
40	CTC AGC GAT GCT GGG CAG TAT CTC TGC CAG GCT GGG GAT GAT TCC AAT Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser Asn 195 200 205	861
45	AGT AAT AAG AAG AAT GCT GAC CTC CAA GTG CTA AAG CCC GAG CCC GAG Ser Asn Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro Glu 210 215 220 225	909
50	CTG GTT TAT GAA GAC CTG AGG GGC TCA GTG ACC TTC CAC TGT GCC CTG Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala Leu 230 235 240	957
55	GGC CCT GAG GTG GCA AAC GTG GCC AAA TTT CTG TGC CGA CAG AGC AGT Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser Ser 245 250 255	1005
60	GGG GAA AAC TGT GAC GTG GTC GTC AAC ACC CTG GGG AAG AGG GCC CCA Gly Glu Asn Cys Asp Val Val Val Asn Thr Leu Gly Lys Arg Ala Pro 260 265 270	1053
65	GCC TTT GAG GGC AGG ATC CTG CTC AAC CCC CAG GAC AAG GAT GGC TCA Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly Ser 275 280 285	1101
70	TTC AGT GTG GTG ATC ACA GGC CTG AGG AAG GAG GAT GCA GGG CGC TAC Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg Tyr 290 295 300 305	1149
75	CTG TGT GGA GCC CAT TCG GAT GGT CAG CTG CAG GAA GGC TCG CCT ATC Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro Ile 310 315 320	1197
80	CAG GCC TGG CAA CTC TTC GTC AAT GAG GAG TCC ACG ATT CCC CGC AGC Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg Ser	1245

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	325	330	335	
5	CCC ACT GTG GTG AAG GGG GTG GCA GGA AGC TCT GTG GCC GTG CTC TGC Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala Val Leu Cys 340 345 350			1293
10	CCC TAC AAC CGT AAG GAA AGC AAA AGC ATC AAG TAC TGG TGT CTC TGG Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp Cys Leu Trp 355 360 365			1341
15	GAA GGG GCC CAG AAT GGC CGC TGC CCC CTG CTG GTG GAC AGC GAG GGG Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp Ser Glu Gly 370 375 380 385			1389
20	TGG GTT AAG GCC CAG TAC GAG GGC CCC CTC TCC CTG CTG GAG GAG CCA Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu Glu Glu Pro 390 395 400			1437
25	GGC AAC GGC ACC TTC ACT GTC ATC CTC AAC CAG CTC ACC AGC CGG GAC Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr Ser Arg Asp 405 410 415			1485
30	GCC GGC TTC TAC TGG TGT CTG ACC AAC GGC GAT ACT CTC TGG AGG ACC Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu Trp Arg Thr 420 425 430			1533
35	ACC GTG GAG ATC AAG ATT ATC GAA GGA GAA CCA AAC CTC AAG GTA CCA Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu Lys Val Pro 435 440 445			1581
40	GGG AAT GTC ACG GCT GTG CTG GGA GAG ACT CTC AAG GTC CCC TGT CAC Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val Pro Cys His 450 455 460 465			1629
45	TTT CCA TGC AAA TTC TCC TCG TAC GAG AAA TAC TGG TGC AAG TGG AAT Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys Lys Trp Asn 470 475 480			1677
50	AAC ACG GGC TGC CAG GCC CTG CCC AGC CAA GAC GAA GGC CCC AGC AAG Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly Pro Ser Lys 485 490 495			1725
55	GCC TTC GTG AAC TGT GAC GAG AAC AGC CGG CTT GTC TCC CTG ACC CTG Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser Leu Thr Leu 500 505 510			1773
60	AAC CTG GTG ACC AGG GCT GAT GAG GGC TGG TAC TGG TGT GGA GTG AAG Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys 515 520 525			1821
65	CAG GGC CAC TTC TAT GGA GAG ACT GCA GCC GTC TAT GTG GCA GTT GAA Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu 530 535 540 545			1869
70	GAG AGG AAG GCA GCG GGG TCC CGC GAT GTC AGC CTA GCG AAG GCA GAC Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala Asp 550 555 560			1917
75	GCT GCT CCT GAT GAG AAG GTG CTA GAC TCT GGT TTT CGG GAG ATT GAG Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg Glu Ile Glu 565 570 575			1965
80	AAC AAA GCC ATT CAG GAT CCC AGG CTT TTT GCA GAG GAA AAG GCG GTG Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala Val 580 585 590			2013

	GCA GAT ACA AGA GAT CAA GCC GAT GGG AGC AGA GCA TCT GTG GAT TCC Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser Val Asp Ser 595 600 605	2061
5	GGC AGC TCT GAG GAA CAA GGT GGA AGC TCC AGA GCG CTG GTC TCC ACC Gly Ser Ser Glu Glu Gln Gly Ser Ser Arg Ala Leu Val Ser Thr 610 615 620 625	2109
10	CTG GTG CCC CTG GGC CTG GTG CTG GCA GTG GGA GCC GTG GCT GTG GGG Leu Val Pro Leu Gly Leu Val Ala Val Gly Ala Val Ala Val Gly 630 635 640	2157
15	GTG GCC AGA GCC CGG CAC AGG AAG AAC GTC GAC CGA GTT TCA ATC AGA Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val Ser Ile Arg 645 650 655	2205
20	AGC TAC AGG ACA GAC ATT AGC ATG TCA GAC TTC GAG AAC TCC AGG GAA Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Glu 660 665 670	2253
25	TTT GGA GCC AAT GAC AAC ATG GGA GCC TCT TCG ATC ACT CAG GAG ACA Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu Thr 675 680 685	2301
30	TCC CTC GGA GGA AAA GAA GAG TTT GTT GCC ACC ACT GAG AGC ACC ACA Ser Leu Gly Gly Lys Glu Glu Phe Val Ala Thr Thr Glu Ser Thr Thr 690 695 700 705	2349
35	GAG ACC AAA GAA CCC AAG AAG GCA AAA AGG TCA TCC AAG GAG GAA GCC Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala 710 715 720	2397
40	GAG ATG GCC TAC AAA GAC TTC CTG CTC CAG TCC AGC ACC GTG GCC GCC Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala Ala 725 730 735	2445
45	GAG GCC CAG GAC GGC CCC CAG GAA GCC TAGACGGTGT CGCCGCCCTGC TCCCTGCA Glu Ala Gln Asp Gly Pro Gln Glu Ala 740 745	2500
50	CCCATGACAA TCACCTTCAG AATCATGTCG ATCCTGGGG CCCTCAGCTC CTGGGGACCC CACTCCCTGC TCTAACACCT GCCTAGTTT TTCTACTGT CCTCAGAGGC GTGCTGGTCC GAGACGTGCA GCGCCCTCT GCACCCCTAT CATGGATGAG AAAGATAGAG GGAGGTCCCCA CTTGCAACTT CTTCTGTTG AGAGAACCTC AGGTACGGAG AAGAATAGAG GTCTCTATGG GTCCCTTGAA GGAAGAGGGA CCAGGGTGGG AGAGCTGATT GCAGAAAGGA ACTCCATCCC TCCCTCCCGT CCTTCCCTC TTCTTCTTC CTTACCATCA AAAGATGTA	2560 2620 2680 2740 2800 2860 2919
55		

(2) INFORMATION FOR SEQ ID NO: 4:

- 60 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 746 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 65 DESCRIPTION: Human Polyimmunoglobulin Receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn
 1 5 10 15

5 Ser Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His
 20 25 30

10 Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr
 35 40 45

15 Leu Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala
 50 55 60

20 Asn Leu Thr Asn Phe Pro Glu Asn Gly Thr Phe Val Val Asn Ile Ala
 65 70 75 80

25 Gln Leu Ser Gln Asp Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile
 85 90 95

30 Asn Ser Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser Gln Gly
 100 105 110

35 Pro Gly Leu Leu Asn Asp Thr Lys Val Tyr Thr Val Asp Leu Gly Arg
 115 120 125

40 Thr Val Thr Ile Asn Cys Pro Phe Lys Thr Glu Asn Ala Gln Lys Arg
 130 135 140

45 Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro Val Leu Val Ile Asp
 145 150 155 160

50 Ser Ser Gly Tyr Val Asn Pro Asn Tyr Thr Gly Arg Ile Arg Leu Asp
 165 170 175

55 Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser Val Val Ile Asn Gln Leu
 180 185 190

60 Arg Leu Ser Asp Ala Gly Gln Tyr Leu Cys Gln Ala Gly Asp Asp Ser
 195 200 205

65 Asn Ser Asn Lys Lys Asn Ala Asp Leu Gln Val Leu Lys Pro Glu Pro
 210 215 220

70 Glu Leu Val Tyr Glu Asp Leu Arg Gly Ser Val Thr Phe His Cys Ala
 225 230 235 240

75 Leu Gly Pro Glu Val Ala Asn Val Ala Lys Phe Leu Cys Arg Gln Ser
 245 250 255

80 Ser Gly Glu Asn Cys Asp Val Val Asn Thr Leu Gly Lys Arg Ala
 260 265 270

85 Pro Ala Phe Glu Gly Arg Ile Leu Leu Asn Pro Gln Asp Lys Asp Gly
 275 280 285

90 Ser Phe Ser Val Val Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly Arg
 290 295 300

95 Tyr Leu Cys Gly Ala His Ser Asp Gly Gln Leu Gln Glu Gly Ser Pro
 305 310 315 320

100 Ile Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro Arg
 325 330 335

105 Ser Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala Val Leu

	340	345	350	
	Cys Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp Cys Leu			
	355	360	365	
5	Trp Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp Ser Glu			
	370	375	380	
10	Gly Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu Glu Glu			
	385	390	395	400
	Pro Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr Ser Arg			
	405	410	415	
15	Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu Trp Arg			
	420	425	430	
	Thr Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu Lys Val			
	435	440	445	
20	Pro Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val Pro Cys			
	450	455	460	
	His Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys Lys Trp			
25	465	470	475	480
	Asn Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly Pro Ser			
	485	490	495	
30	Lys Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser Leu Thr			
	500	505	510	
	Leu Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys Gly Val			
	515	520	525	
35	Lys Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val			
	530	535	540	
	Glu Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala			
40	545	550	555	560
	Asp Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg Glu Ile			
	565	570	575	
45	Glu Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala			
	580	585	590	
	Val Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser Val Asp			
	595	600	605	
50	Ser Gly Ser Ser Glu Glu Gln Gly Ser Ser Arg Ala Leu Val Ser			
	610	615	620	
	Thr Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Val Ala Val			
55	625	630	635	640
	Gly Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val Ser Ile			
	645	650	655	
60	Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg			
	660	665	670	
	Glu Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu			
	675	680	685	
65	Thr Ser Leu Gly Gly Lys Glu Glu Phe Val Ala Thr Thr Glu Ser Thr			

690	695	700														
Thr	Glu	Thr	Lys	Glu	Pro	Lys	Lys	Ala	Lys	Arg	Ser	Ser	Lys	Glu	Glu	
705					710					715					720	
5																
	Ala	Glu	Met	Ala	Tyr	Lys	Asp	Phe	Leu	Leu	Gln	Ser	Ser	Thr	Val	Ala
					725					730					735	
10	Ala	Glu	Ala	Gln	Asp	Gly	Pro	Gln	Glu	Ala						
					740				745							

15 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	3630 base pairs
20	(B)	TYPE: nucleic acid
	(C)	STRANDEDNESS: single
	(D)	TOPOLOGY: linear
		DESCRIPTION: Bovine Polyimmunoglobulin Receptor

25 (ix) FEATURE:

(A)	NAME/KEY:	Coding Sequence
20	(B)	LOCATION: 152....2425

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GATCTCCTCG	GAGGGTCGTG	CAGCGGCCCT	GGGTCCCTGC	CGGCACCAAGT	ACTTGCGCGT	60	
30							
	GTGCTCCCAA	AGCTGACGGG	ATAGGAGGAA	GGAGCTCAAA	CAACCACACA	GGACGGTGGC	120
35	TGGCGGCAGA	GACCCGCGGG	AGCCCCCAGC	G ATG TCG CGC CTG TTC CTC GCC	Met Ser Arg Leu Phe Leu Ala		172
				1	5		
40	TGC CTG CTG GCC ATC TTC CCA GTG GTC TCC ATG AAG AGT CCC ATC TTC	Cys Leu Leu Ala Ile Phe Pro Val Val Ser Met Lys Ser Pro Ile Phe	220				
	10	15	20				
45	GGT CCC GAG GAG GTG AGC AGC GTG GAA GGC CGC TCA GTG TCC ATC AAG	Gly Pro Glu Glu Val Ser Ser Val Glu Gly Arg Ser Val Ser Ile Lys	268				
	25	30	35				
50	TGC TAC TAC CCG CCC ACC TCC GTC AAC CGG CAC ACG CGC AAG TAC TGG	Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp	316				
	40	45	50	55			
55	TGC CGG CAG GGA GCC CAG GGC CGC TGC ACG ACC CTC ATC TCC TCG GAG	Cys Arg Gln Gly Ala Gln Gly Arg Cys Thr Thr Leu Ile Ser Ser Glu	364				
	60	65	70				
60	GGC TAC GTC TCC GAC GAC TAC GTG GGC AGA GCC AAC CTC ACC AAC TTC	Gly Tyr Val Ser Asp Asp Tyr Val Gly Arg Ala Asn Leu Thr Asn Phe	412				
	75	80	85				
65	CCG GAG AGC GGC ACG TTT GTG GTG GAC ATC AGC CAT CTC ACC CAT AAA	Pro Glu Ser Gly Thr Phe Val Val Asp Ile Ser His Leu Thr His Lys	460				
	90	95	100				
70	GAC TCA GGG CGC TAC AAG TGT GGC CTG GGC ATT AGC AGC CGT GGC CTT	Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Ser Ser Arg Gly Leu	508				
	105	110	115				

	AAC TTC GAT GTG AGC CTG GAG GTC AGC CAA GAT CCT GCA CAG CCA AGT Asn Phe Asp Val Ser Leu Glu Val Ser Gln Asp Pro Ala Gln Ala Ser 120	125	130	135	556
5	CAT GCC CAC GTC TAC ACT ATA GAC CTG GGC AGG ACT GTG ACC ATC AAC His Ala His Val Tyr Thr Ile Asp Leu Gly Arg Thr Val Thr Ile Asn 140	145	150		604
10	TGC CCT TTC ACG CGT GCG AAT TCT GAG AAG AGA AAA TCC TTG TGC AAG Cys Pro Phe Thr Arg Ala Asn Ser Glu Lys Arg Lys Ser Leu Cys Lys 155	160	165		652
15	AAG ACA ATC CAG GAC TGT TTC CAA GTT GTC GAC TCC ACC GGG TAT GTG Lys Thr Ile Gln Asp Cys Phe Gln Val Val Asp Ser Thr Gly Tyr Val 170	175	180		700
20	AGC AAC AGC TAT AAA GAC AGA GCA CAT ATC AGT ATC CTA GGT ACC AAC Ser Asn Ser Tyr Lys Asp Arg Ala His Ile Ser Ile Leu Gly Thr Asn 185	190	195		748
25	ACA TTA GTG TTC AGC GTT GTC ATC AAC CGA GTC AAG CTC AGT GAT GCT Thr Leu Val Phe Ser Val Val Ile Asn Arg Val Lys Leu Ser Asp Ala 200	205	210	215	796
30	GGG ATG TAT GTC TGC CAG GCT GGG GAC GAT GCC AAA GCC GAT AAA ATC Gly Met Tyr Val Cys Gln Ala Gly Asp Asp Ala Lys Ala Asp Lys Ile 220	225	230		844
35	AAC ATT GAC CTC CAG GTG CTG GAG CCT GAG CCT GAG CTG GTT TAT GGA Asn Ile Asp Leu Gln Val Leu Glu Pro Glu Pro Glu Leu Val Tyr Gly 235	240	245		892
40	GAC TTG AGG AGC TCG GTG ACC TTT GAC TGT TCC CTG GGC CCC GAG GTG Asp Leu Arg Ser Ser Val Thr Phe Asp Cys Ser Leu Gly Pro Glu Val 250	255	260		940
45	GCA AAT GTG CCC AAA TTT CTG TGC CAG AAG AAG AAT GGG GGA GCT TGC Ala Asn Val Pro Lys Phe Leu Cys Gln Lys Lys Asn Gly Gly Ala Cys 265	270	275		988
50	AAT GTA GTC ATC AAC ACG TTG GGG AAG AAG GCT CAG GAC TTC CAG GGC Asn Val Val Ile Asn Thr Leu Gly Lys Lys Ala Gln Asp Phe Gln Gly 280	285	290	295	1036
55	AGG ATC GTG TCC GTG CCC AAG GAC AAT GGT GTC TTC AGT GTG CAC ATT Arg Ile Val Ser Val Pro Lys Asp Asn Gly Val Phe Ser Val His Ile 300	305	310		1084
60	ACC AGC CTG AGG AAA GAG GAC GCA GGG CGC TAC GTG TGC GGG GCC CAG Thr Ser Leu Arg Lys Glu Asp Ala Gly Arg Tyr Val Cys Gly Ala Gln 315	320	325		1132
65	CCT GAG GGT GAG CCC CAG GAC GGC TGG CCT GTG CAG GCC TGG CAA CTC Pro Glu Gly Glu Pro Gln Asp Gly Trp Pro Val Gln Ala Trp Gln Leu 330	335	340		1180
70	TTC GTC AAT GAA GAG ACG GCA ATC CCC GCA AGC CCC TCC GTG GTG AAA Phe Val Asn Glu Glu Thr Ala Ile Pro Ala Ser Pro Ser Val Val Lys 345	350	355		1228
75	GGT GTG AGG GGA GGC TCT GTG ACT GTA TCT TGC CCC TAC AAC CCT AAG Gly Val Arg Gly Gly Ser Val Thr Val Ser Cys Pro Tyr Asn Pro Lys 360	365	370	375	1276
80	GAT GCC AAC AGC GCG AAG TAC TGG TGT CAC TGG GAA GAG GCT CAA AAC Asp Ala Asn Ser Ala Lys Tyr Trp Cys His Trp Glu Glu Ala Gln Asn 385	390	395		1324

	380	385	390	
5	GGC CGC TGC CCG CGG CTG GTG GAG AGC CGG GGG CTG ATG AAG GAG CAG Gly Arg Cys Pro Arg Leu Val Glu Ser Arg Gly Leu Met Lys Glu Gln 395 400 405			1372
10	TAC GAG GGC AGG CTG GTG CTG CTC ACC GAG CCG GGC AAC GGC ACC TAC Tyr Glu Gly Arg Leu Val Leu Leu Thr Glu Pro Gly Asn Gly Thr Tyr 410 415 420			1420
15	ACC GTC ATC CTC AAC CAG CTC ACC GAT CAG GAC GCC GGC TTC TAC TGG Thr Val Ile Leu Asn Gln Leu Thr Asp Gln Asp Ala Gly Phe Tyr Trp 425 430 435			1468
20	TGC GTG ACC GAC GGC GAC ACG CGC TGG ATC TCC ACA GTG GAG CTC AAG Cys Val Thr Asp Gly Asp Thr Arg Trp Ile Ser Thr Val Glu Leu Lys 440 445 450 455			1516
25	GTT GTC CAA GGA GAA CCA AGC CTC AAG GTA CCC AAG AAC GTC ACG GCT Val Val Gln Gly Glu Pro Ser Leu Lys Val Pro Lys Asn Val Thr Ala 460 465 470			1564
30	TGG CTG GGA GAG CCC TTA AAG CTC TCC TGC CAC TTC CCC TGC AAA TTC Trp Leu Gly Glu Pro Leu Lys Leu Ser Cys His Phe Pro Cys Lys Phe 475 480 485			1612
35	TAC TCC TTT GAG AAG TAC TGG TGT AAG TGG AGC AAC AGA GGC TGC AGC Tyr Ser Phe Glu Lys Tyr Trp Cys Lys Trp Ser Asn Arg Gly Cys Ser 490 495 500			1660
40	GCC CTG CCC ACC CAG AAC GAC GGC CCC AGC CAG GCC TTT GTG AGC TGC Ala Leu Pro Thr Gln Asn Asp Gly Pro Ser Gln Ala Phe Val Ser Cys 505 510 515			1708
45	GAC CAG AAC AGC CAG GTC GTC TCC CTG AAC CTG GAC ACA GTC ACC AAG Asp Gln Asn Ser Gln Val Val Ser Leu Asn Leu Asp Thr Val Thr Lys 520 525 530 535			1756
50	GAG GAT GAA GGC TGG TAC TGG TGT GGA GTG AAG GAA GGC CCC CGA TAC Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Pro Arg Tyr 540 545 550			1804
55	GGG GAG ACG GCG GCT GTC TAC GTG GCA GTG GAG AGC AGG GTG AAG GGG Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu Ser Arg Val Lys Gly 555 560 565			1852
60	TCC CAA GGC GCC AAG CAA GTG AAA GCT GCC CCT GCG GGG GCG GCA ATA Ser Gln Gly Ala Lys Gln Val Lys Ala Ala Pro Ala Gly Ala Ala Ile 570 575 580			1900
65	CAG TCG AGG GCC GGG GAG ATC CAG AAC AAA GCC CTT CTG GAC CCC AGC Gln Ser Arg Ala Gly Glu Ile Gln Asn Lys Ala Leu Leu Asp Pro Ser 585 590 595			1948
70	TTT TTC GCA AAG GAA AGT GTG AAG GAC GCT GCT GGT GGA CCC GGA GCA Phe Phe Ala Lys Glu Ser Val Lys Asp Ala Ala Gly Gly Pro Gly Ala 600 605 610 615			1996
75	CCT GCA GAT CCT GGC CGC CCT ACA GGA TAC AGC GGG AGC TCC AAA GCA Pro Ala Asp Pro Gly Arg Pro Thr Gly Tyr Ser Gly Ser Ser Lys Ala 620 625 630			2044
80	CTG GTC TCC ACC CTG GTG CCC CTG GCC CTG GTC CTG GTC GCA GGG GTC Leu Val Ser Thr Leu Val Pro Leu Ala Leu Val Leu Val Ala Gly Val 635 640 645			2092

	GTG GCG ATC GGG GTG GTC CGA GCC CGG CAC AGG AAG AAC GTC GAC CGG Val Ala Ile Gly Val Val Arg Ala Arg His Arg Lys Asn Val Asp Arg 650 655 660	2140
5	ATT TCA ATC AGG AGC TAC CGG ACA GAT ATC AGC ATG TCA GAC TTT GAG Ile Ser Ile Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu 665 670 675	2188
10	AAC TCC AGG GAT TTT GAA GGA CGT GAC AAC ATG GGA GCC TCT CCA GAG Asn Ser Arg Asp Phe Glu Gly Arg Asp Asn Met Gly Ala Ser Pro Glu 680 685 690 695	2236
15	GCC CAA GAG ACG TCT CTC GGA GGG AAG GAC GAG TTT GCC ACC ACT ACC Ala Gln Glu Thr Ser Leu Gly Gly Lys Asp Glu Phe Ala Thr Thr Thr 700 705 710	2284
20	GAG GAC ACC GTG GAG ACC AAA GAA CCC AAG AAG GCA AAG AGG TCG TCC Glu Asp Thr Val Glu Ser Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser 715 720 725	2332
25	AAG GAG GAA GCC GAC GAG GCC TTC ACC ACC TTC CTC CTC CAG GCC AAA Lys Glu Ala Asp Glu Ala Phe Thr Thr Phe Leu Leu Gln Ala Lys 730 735 740	2380
30	AAC CTG GCC TCC GCC GCA ACC CAG AAC GGC CCG ACA GAA GCC TAG ACGGAG Asn Leu Ala Ser Ala Ala Thr Gln Asn Gly Pro Thr Glu Ala 745 750 755	2431
35	CCCTGGCGC CCCTTCCCTC CGCACGTGGC AATCACGCTC CGAACATCACGC TGATCCTCAG GGCCCTCAGC TCGGGGGGCT CCACTGCCTG CACTCACACC CGGCCTAGGC TTCTCCTGTC TGTCTCAGA GGGTGTGCTG GTTCCTTCTT GGTGGCATCC AAGCCTGGCT TACTTGTTC TATTGGGGGT GAGGTGGTAC GAGGAGTTCC CACCTGCAGC TTATTCGAAC GAGAGAACTA AAGGTGTGGA GGAGAATTAA GATGCCAGAG GGGCCTCTCA GAAAGAAAAG GAGTGGGTGG GGAGACAACC GCAGAAAGGG GGCCATTCA CGCTTCCCTG TCCCCTTATT TGGGGATGTC 40 AGTGGATCC TCCCTTCCAC CCCATCTCTG CACCTCTCCA TCCCCACTCC ATTCCATCTT CTCTTCTTCT TTCCCTCATT AAAAATGTGC ATTTGGTTAC TCACTAGATT CCAGGGACTC TGCTAGACAC TGGGATAGGT AGGCCGCAAT CCCAGGGGGC AGCCTTCCGC AACATCAAG GAGCCCTGG AGCCCACAGC ATCTCTTCAC GTGTACACTC ACTGACCTCT GCCTCTGCTG GGAGAAATCA TAAAGGGTCT GCAGCCCTGA GGCCTTAGGG ATTATGTAAC ACAGGCATAC 50 ACACAAGGCA CCATCAACAC ATTCTTACCA TTTCACAGGT GAGAAAGCCG AGGTCTGAG AGGTGGAGAG GTTGCTCAG AGTCAGCAAG TGAGATGTAC GAGTCTCAAG CTAAAGATTT GACACCTGCT GTCCCTACAG GAGGGCTCC TCTCTCCAGA TGAGACAGCA TTCCATAGGA AGGAGAAGAA AAATGTAAT AAGACTGGTC TTTCACAGGC CCCACATCAG GGAAGATA 60 CCTTTCCCTG TCTGTCACTC ACAGAGACCT AATAGGATAA GAGAATGGTC AACACTCAA CCCCCGAATG TGAAGAGTTC TAAGTGGAAA GGGAGGAAAA AGGGGGGATT TGATGGTGC AGGGAGGGC TGATCTCCAA AGAACTAAGG TTTAAGTTTT TTTGTTTTT TTTTCCTTC 65 TTCTAAGCTC TGCACCTCAA CTAGCATCTA TGAGCTGGCA CTTGCTAACAA AATCAAAAT	2491 2551 2611 2671 2731 2791 2851 2911 2971 3031 3091 3151 3211 3271 3331 3391 3451 3511 3571

THE SEQUENCING PROJECT

GTGAATTAAT TAATAATTAA AGACCATGAT TTCCCTCCAAA AAAAAAAA AAAAAAAA

3630

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 757 amino acids
 (B) TYPE: amino acid
 (C) STRANNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Bovine Polyimmunoglobulin Receptor

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Ser	Arg	Leu	Phe	Leu	Ala	Cys	Leu	Leu	Ala	Ile	Phe	Pro	Val	Val	
1					5				10					15		
20	Ser	Met	Lys	Ser	Pro	Ile	Phe	Gly	Pro	Glu	Glu	Val	Ser	Ser	Val	Glu
					20				25					30		
25	Gly	Arg	Ser	Val	Ser	Ile	Lys	Cys	Tyr	Tyr	Pro	Pro	Thr	Ser	Val	Asn
						35		40					45			
30	Arg	His	Thr	Arg	Lys	Tyr	Trp	Cys	Arg	Gln	Gly	Ala	Gln	Gly	Arg	Cys
						50		55				60				
35	Thr	Thr	Leu	Ile	Ser	Ser	Glu	Gly	Tyr	Val	Ser	Asp	Asp	Tyr	Val	Gly
						65		70		75		80				
40	Arg	Ala	Asn	Leu	Thr	Asn	Phe	Pro	Glu	Ser	Gly	Thr	Phe	Val	Val	Asp
						85			90			95				
45	Ile	Ser	His	Leu	Thr	His	Lys	Asp	Ser	Gly	Arg	Tyr	Lys	Cys	Gly	Leu
						100		105				110				
50	Gly	Ile	Ser	Ser	Arg	Gly	Leu	Asn	Phe	Asp	Val	Ser	Leu	Glu	Val	Ser
						115		120				125				
55	Gln	Asp	Pro	Ala	Gln	Ala	Ser	His	Ala	His	Val	Tyr	Thr	Ile	Asp	Leu
						130		135			140					
60	Gly	Arg	Thr	Val	Thr	Ile	Asn	Cys	Pro	Phe	Thr	Arg	Ala	Asn	Ser	Glu
						145		150			155			160		
65	Lys	Arg	Lys	Ser	Leu	Cys	Lys	Lys	Thr	Ile	Gln	Asp	Cys	Phe	Gln	Val
						165			170			175				
70	Val	Asp	Ser	Thr	Gly	Tyr	Val	Ser	Asn	Ser	Tyr	Lys	Asp	Arg	Ala	His
						180			185			190				
75	Ile	Ser	Ile	Leu	Gly	Thr	Asn	Thr	Leu	Val	Phe	Ser	Val	Val	Ile	Asn
						195			200			205				
80	Arg	Val	Lys	Leu	Ser	Asp	Ala	Gly	Met	Tyr	Val	Cys	Gln	Ala	Gly	Asp
						210			215			220				
85	Asp	Ala	Lys	Ala	Asp	Lys	Ile	Asn	Ile	Asp	Leu	Gln	Val	Leu	Glu	Pro
						225			230			235			240	
90	Glu	Pro	Glu	Leu	Val	Tyr	Gly	Asp	Leu	Arg	Ser	Ser	Val	Thr	Phe	Asp
						245			250			255				
95	Cys	Ser	Leu	Gly	Pro	Glu	Val	Ala	Asn	Val	Pro	Lys	Phe	Leu	Cys	Gln
						260			265			270				

Lys Lys Asn Gly Gly Ala Cys Asn Val Val Ile Asn Thr Leu Gly Lys
 275 280 285

5 Lys Ala Gln Asp Phe Gln Gly Arg Ile Val Ser Val Pro Lys Asp Asn
 290 295 300

Gly Val Phe Ser Val His Ile Thr Ser Leu Arg Lys Glu Asp Ala Gly
 305 310 315 320

10 Arg Tyr Val Cys Gly Ala Gln Pro Glu Gly Glu Pro Gln Asp Gly Trp
 325 330 335

Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Thr Ala Ile Pro
 340 345 350

15 Ala Ser Pro Ser Val Val Lys Gly Val Arg Gly Gly Ser Val Thr Val
 355 360 365

Ser Cys Pro Tyr Asn Pro Lys Asp Ala Asn Ser Ala Lys Tyr Trp Cys
 20 370 375 380

His Trp Glu Glu Ala Gln Asn Gly Arg Cys Pro Arg Leu Val Glu Ser
 385 390 395 400

25 Arg Gly Leu Met Lys Glu Gln Tyr Glu Gly Arg Leu Val Leu Leu Thr
 405 410 415

Glu Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Asp
 420 425 430

30 Gln Asp Ala Gly Phe Tyr Trp Cys Val Thr Asp Gly Asp Thr Arg Trp
 435 440 445

Ile Ser Thr Val Glu Leu Lys Val Val Gln Gly Glu Pro Ser Leu Lys
 35 450 455 460

Val Pro Lys Asn Val Thr Ala Trp Leu Gly Glu Pro Leu Lys Leu Ser
 465 470 475 480

40 Cys His Phe Pro Cys Lys Phe Tyr Ser Phe Glu Lys Tyr Trp Cys Lys
 485 490 495

Trp Ser Asn Arg Gly Cys Ser Ala Leu Pro Thr Gln Asn Asp Gly Pro
 500 505 510

45 Ser Gln Ala Phe Val Ser Cys Asp Gln Asn Ser Gln Val Val Ser Leu
 515 520 525

Asn Leu Asp Thr Val Thr Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly
 50 530 535 540

Val Lys Glu Gly Pro Arg Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala
 545 550 555 560

55 Val Glu Ser Arg Val Lys Gly Ser Gln Gly Ala Lys Gln Val Lys Ala
 565 570 575

Ala Pro Ala Gly Ala Ala Ile Gln Ser Arg Ala Gly Glu Ile Gln Asn
 580 585 590

60 Lys Ala Leu Leu Asp Pro Ser Phe Phe Ala Lys Glu Ser Val Lys Asp
 595 600 605

Ala Ala Gly Gly Pro Gly Ala Pro Ala Asp Pro Gly Arg Pro Thr Gly
 65 610 615 620

Tyr Ser Gly Ser Ser Lys Ala Leu Val Ser Thr Leu Val Pro Leu Ala
 625 630 635 640
 5 Leu Val Leu Val Ala Gly Val Val Ala Ile Gly Val Val Arg Ala Arg
 645 650 655
 His Arg Lys Asn Val Asp Arg Ile Ser Ile Arg Ser Tyr Arg Thr Asp
 660 665 670
 10 Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Asp Phe Glu Gly Arg Asp
 675 680 685
 Asn Met Gly Ala Ser Pro Glu Ala Gln Glu Thr Ser Leu Gly Gly Lys
 690 695 700
 15 Asp Glu Phe Ala Thr Thr Glu Asp Thr Val Glu Ser Lys Glu Pro
 705 710 715 720
 20 Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Glu Ala Phe Thr
 725 730 735
 Thr Phe Leu Leu Gln Ala Lys Asn Leu Ala Ser Ala Ala Thr Gln Asn
 740 745 750
 25 Gly Pro Thr Glu Ala
 755

30

(2) INFORMATION FOR SEQ ID NO: 7:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3095 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 DESCRIPTION: Mouse Polyimmunoglobulin Receptor

(ix) FEATURE:

45 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 85....2400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

50 TCACCTGGAG AGAAGGAAGT AGCTAAAACA TTCTCATACA AGAAGCCAAC CTGAGCGGCA 60
 CAGCCCCCCT GGAAGCCACA AGCA ATG AGG CTC TAC TTG TTC ACG CTC TTG
 Met Arg Leu Tyr Leu Phe Thr Leu Leu
 1 5
 55 GTA ACT GTC TTT TCA GGG GTC TCC ACA AAA AGC CCC ATA TTT GGT CCC 159
 Val Thr Val Phe Ser Gly Val Ser Thr Lys Ser Pro Ile Phe Gly Pro
 10 15 20 25
 60 CAG GAG GTG AGT AGT ATA GAA GGC GAC TCT GTT TCC ATC ACG TGC TAC 207
 Gln Glu Val Ser Ser Ile Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
 30 35 40
 65 TAC CCA GAC ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA 255
 Tyr Pro Asp Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg
 45 50 55

	CAA GGA GCC AGC GGC ATG TGC ACA ACG CTC ATC TCT TCA AAT GGC TAC Gln Gly Ala Ser Gly Met Cys Thr Thr Leu Ile Ser Ser Asn Gly Tyr 60 65 70	303
5	CTC TCC AAG GAG TAT TCA GGC AGA GCC AAC CTC ATC AAC TTC CCA GAG Leu Ser Lys Glu Tyr Ser Gly Arg Ala Asn Leu Ile Asn Phe Pro Glu 75 80 85	351
10	AAC AAC ACA TTT GTG ATT AAC ATT GAG CAG CTC ACC CAG GAC GAC ACT Asn Asn Thr Phe Val Ile Asn Ile Glu Gln Leu Thr Gln Asp Asp Thr 90 95 100 105	399
15	GGG AGC TAC AAG TGT GGC CTG GGT ACC AGT AAC CGA GGC CTG TCC TTC Gly Ser Tyr Lys Cys Gly Leu Gly Thr Ser Asn Arg Gly Leu Ser Phe 110 115 120	447
20	GAT GTC AGC CTG GAG GTC AGC CAG GTT CCT GAG TTG CCG AGT GAC ACC Asp Val Ser Leu Glu Val Ser Gln Val Pro Glu Leu Pro Ser Asp Thr 125 130 135	495
25	CAC GTC TAC ACA AAG GAC ATA GGC AGA AAT GTG ACC ATT GAA TGC CCT His Val Tyr Thr Lys Asp Ile Gly Arg Asn Val Thr Ile Glu Cys Pro 140 145 150	543
30	TTC AAA AGG GAG AAT GTT CCC AGC AAG AAA TCC CTG TGT AAG AAG ACA Phe Lys Arg Glu Asn Val Pro Ser Lys Ser Leu Cys Lys Lys Thr 155 160 165	591
35	AAC CAG TCC TGC GAA CTT GTC ATT GAC TCT ACT GAG AAG GTG AAC CCC Asn Gln Ser Cys Glu Leu Val Ile Asp Ser Thr Glu Lys Val Asn Pro 170 175 180 185	639
40	AGC TAT ATA GGC AGA GCA AAA CTT TTT ATG AAA GGG ACC GAC CTA ACT Ser Tyr Ile Gly Arg Ala Lys Leu Phe Met Lys Gly Thr Asp Leu Thr 190 195 200	687
45	GTA TTC TAT GTC AAC ATT AGT CAC CTA ACG CAC AAT GAT GCT GGG CTG Val Phe Tyr Val Asn Ile Ser His Leu Thr His Asn Asp Ala Gly Leu 205 210 215	735
50	TAC ATC TGC CAA GCT GGA GAA GGT CCT AGT GCT GAT AAG AAG AAT GTT Tyr Ile Cys Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Lys Asn Val 220 225 230	783
55	GAC CTC CAG GTG CTA GCG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG Asp Leu Gln Val Leu Ala Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu 235 240 245	831
60	AGG TCC TCA GTG ACT TTT GAA TGT GAC CTG GGC CGT GAG GTG GCA AAC Arg Ser Ser Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn 250 255 260 265	879
65	GAG GCC AAA TAT CTG TGC CGG ATG AAT AAG GAA ACC TGT GAT GTG ATC Glu Ala Lys Tyr Leu Cys Arg Met Asn Lys Glu Thr Cys Asp Val Ile 270 275 280	927
	ATT AAC ACC CTG GGG AAG AGG GAT CCA GAC TTT GAG GGC AGG ATC CTG Ile Asn Thr Leu Gly Lys Arg Asp Pro Asp Phe Glu Gly Arg Ile Leu 285 290 295	975
	ATA ACC CCC AAG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC Ile Thr Pro Lys Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly 300 305 310	1023
	CTG AGG AAG GAG GAT GCA GGG CAC TAC CAG TGT GGA GCC CAC AGT TCT Leu Arg Lys Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser	1071

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	315	320	325	
5	GGT TTG CCT CAA GAA GGC TGG CCC ATC CAG ACT TGG CAA CTC TTT GTC Gly Leu Pro Gln Glu Gly Trp Pro Ile Gln Thr Trp Gln Leu Phe Val 330 335 340 345			1119
10	AAT GAA GAG TCT ACC ATT CCC AAT CGT CGC TCT GTT GTG AAG GGA GTC Asn Glu Glu Ser Thr Ile Pro Asn Arg Arg Ser Val Val Lys Gly Val 350 355 360			1167
15	ACA GGA GGC TCT GTG GCC ATC GCC TGT CCC TAT AAC CCC AAG GAA AGC Thr Gly Gly Ser Val Ala Ile Ala Cys Pro Tyr Asn Pro Lys Glu Ser 365 370 375			1215
20	AGC AGC CTC AAG TAC TGG TGT CGC TGG GAA GGG GAC GGA AAT GGA CAT Ser Ser Leu Lys Tyr Trp Cys Arg Trp Glu Gly Asp Gly Asn Gly His 380 385 390			1263
25	TGC CCC GCG CTT GTG GGG ACC CAG GCC CAG GTG CAA GAA GAG TAT GAA Cys Pro Ala Leu Val Gly Thr Gln Ala Gln Val Gln Glu Glu Tyr Glu 395 400 405			1311
30	GGC CGA CTG GCA CTG TTT GAT CAG CCA GGC AAT GGT ACT TAC ACT GTC Gly Arg Leu Ala Leu Phe Asp Gln Pro Gly Asn Gly Thr Tyr Thr Val 410 415 420 425			1359
35	ATC CTC AAC CAG CTC ACC ACC GAG GAT GCT GGC TTC TAT TGG TGT CTT Ile Leu Asn Gln Leu Thr Thr Glu Asp Ala Gly Phe Tyr Trp Cys Leu 430 435 440			1407
40	ACC AAT GGT GAC TCT CGC TGG AGA ACC ACA ATA GAA CTC CAG GTT GCC Thr Asn Gly Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala 445 450 455			1455
45	GAA GCT ACA AGG GAG CCA AAC CTT GAG GTG ACG CCA CAG AAC GCA ACA Glu Ala Thr Arg Glu Pro Asn Leu Glu Val Thr Pro Gln Asn Ala Thr 460 465 470			1503
50	GCA GTA CTA CGA GAG ACC TTC ACC GTT TCC TGC CAC TAT CCG TGC AAA Ala Val Leu Gly Glu Thr Phe Thr Val Ser Cys His Tyr Pro Cys Lys 475 480 485			1551
55	TTC TAC TCC CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC AAG GGT TGC Phe Tyr Ser Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Lys Gly Cys 490 495 500 505			1599
60	CAC ATC CTG CCA AGC CAT GAC GAA GGT GCC CGC CAA TCT TCT GTG AGC His Ile Leu Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser 510 515 520			1647
65	TGC GAC CAG AGC AGC CAG CTG GTC TCC ATG ACC CTG AAC CCG GTC AGT Cys Asp Gln Ser Ser Gln Leu Val Ser Met Thr Leu Asn Pro Val Ser 525 530 535			1695
70	AAG GAA GAT GAA GGC TGG TAC TGG TGT GGG GTA AAG CAA GGC CAG ACC Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Gln Gly Gln Thr 540 545 550			1743
75	TAT GGA GAA ACT ACC GCC ATC TAT ATA GCA GTT GAA GAG AGG ACC AGA Tyr Gly Glu Thr Thr Ala Ile Tyr Ile Ala Val Glu Glu Arg Thr Arg 555 560 565			1791
80	GGG TCA TCC CAT GTC AAC CCA ACA GAT GCA AAT GCA CGT GCC AAA GTC Gly Ser Ser His Val Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Val 570 575 580 585			1839

	GCT CTG GAA GAA GAG GTA GTG GAC TCC TCC ATC AGT GAA AAA GAG AAC Ala Leu Glu Glu Glu Val Val Asp Ser Ser Ile Ser Glu Lys Glu Asn 590 595 600	1887
5	AAA GCC ATT CCA AAT CCC GGG CCT TTT GCC AAC GAA AGA GAG ATA CAG. Lys Ala Ile Pro Asn Pro Gly Pro Phe Ala Asn Glu Arg Glu Ile Gln 605 610 615	1935
10	AAT GTG AGA GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG GAT GCT GGC Asn Val Arg Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asp Ala Gly 620 625 630	1983
15	AGT GCT GAT GGA CAA AGC AGG AGC TCC AGC TCC AAA GTG CTG TTC TCC Ser Ala Asp Gly Gln Ser Arg Ser Ser Ser Lys Val Leu Phe Ser 635 640 645	2031
20	ACC CTG GTG CCC CTG GGT CTG GTG CTG GCA GTG GGT GCT ATA GCT GTG Thr Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Ile Ala Val 650 655 660 665	2079
25	TGG GTG GCC AGA GTC CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC Trp Val Ala Arg Val Arg His Arg Lys Asn Val Asp Arg Met Ser Ile 670 675 680	2127
30	AGC AGC TAC AGG ACA GAC ATT AGC ATG GCA GAC TTC AAG AAC TCC AGA Ser Ser Tyr Arg Thr Asp Ile Ser Met Ala Asp Phe Lys Asn Ser Arg 685 690 695	2175
35	GAT TTG GGA GGC AAT GAC AAC ATG GGG GCC TCT CCA GAC ACA CAG CAA Asp Leu Gly Gly Asn Asp Asn Met Gly Ala Ser Pro Asp Thr Gln Gln 700 705 710	2223
40	ACA GTC ATC GAA GGA AAA GAT GAA ATC GTG ACT ACC ACG GAG TGC ACC Thr Val Ile Glu Gly Lys Asp Glu Ile Val Thr Thr Glu Cys Thr 715 720 725	2271
45	GCT GAG CCA GAA GAA TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA Ala Glu Pro Glu Glu Ser Lys Ala Lys Arg Ser Ser Lys Glu Glu 730 735 740 745	2319
50	GCT GAC ATG GCC TAC TCG GCA TTC CTG CTT CAG TCC AGC ACC ATA GCT Ala Asp Met Ala Tyr Ser Ala Phe Leu Leu Gln Ser Ser Thr Ile Ala 750 755 760	2367
55	GCA CAG CTC CAC GAT GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCCACCC Ala Gln Val His Asp Gly Pro Gln Glu Ala 765 770	2420
60	TTGCCTGTGA CAATCAACTT GAGAATCACA CTGATCCGCT CGCAGCCCAC ACTCACCCAT CACCTCCGCT CTTCCCTCCT GTCCTCAGAG GTGTGCTGGT TCCTTCCTCG GCCATGGAAG CCTGGCCTAG TTACGCCGT TTAGGAGAGA GTGTGAGGCG TTCTTTCTC TATGAAGAGA GTGAGGTGGA AATGAGGAGG AGGTGAAACCT GAGAGACATC TCTGGAGGAA GAGGGTTGAG AATAGGGCT CGTTTCAGGA GAAAAGGCCA TTTGAATCTT CTTTATAACC ATATGATAGG ATGTCAGCGT AACTCTTCTC TCCTCCATCT CTCCTTCCT ATCCTCTTGA TTCAAACAAAC ACATCTGAGA ACTCACTAGG CTTCA GTGCC TACTAAATGC TGAGAGCCAG GCCACAATCT TTCTATAAAAT ATTACTGGAA GAGATGCCAT CTCCTCCCAG ATTCTGTCTT TTCATTAAGA TAAGACATCA TTACCAGGCA TACCTCCTGC CTCTGTGCCT CATAGGCATA CACAAGCCAT	2480 2540 2600 2660 2720 2780 2840 2900 2960
65		

AAGGGCATCA	TGATTTCTAG	ATGAGAAGAG	ATGTTTCTCA	AGAGTGCCTA	GTGAGATAGA	3020
CTAGCGTCAA	ACCAGATGTG	GCAACTCCTG	GCTCTTGGCC	TACGATCTGT	CTTCAGAGAAA	3080
5	AAAAAAAAAA	AAAAA				3095

10 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Arg Leu Tyr Leu Phe Thr Leu Leu Val Thr Val Phe Ser Gly Val
1 5 10 15

Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
35 40 45

30 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Ser Gly Met Cys
50 55 60

Thr Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
65 70 75 80

Arg Ala Asn Leu Ile Asn Phe Pro Glu Asn Asn Thr Phe Val Ile Asn
85 90 95

40 Ile Glu Gln Leu Thr Gln Asp Asp Thr Gly Ser Tyr Lys Cys Gly Leu
100 105 110

Gly Thr Ser Asn Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
115 120 125

45 Gln Val Pro Glu Leu Pro Ser Asp Thr His Val Tyr Thr Lys Asp Ile
130 135 140

Gly Arg Asn Val Thr Ile Glu Cys Pro Phe Lys Arg Glu Asn Val Pro
145 150 155 160

Ser Lys Lys Ser Leu Cys Lys Lys Thr Asn Gln Ser Cys Glu Leu Val
165 170 175

Ile Asp Ser Thr Glu Lys Val Asn Pro Ser Tyr Ile Gly Arg Ala Lys
180 185 190

Leu Phe Met Lys Gly Thr Asp Leu Thr Val Phe Tyr Val Asn Ile Ser
195 200 205

His Leu Thr His Asn Asp Ala Gly Leu Tyr Ile Cys Gin Ala Gly Glu
212 215 218 220

Gly Pro Ser Ala Asp Lys Lys Asn Val Asp Leu Gln Val Leu Ala Pro
225 230 235 240

Glu Pro Glu Lys Lys Thr Lys Asp Lys Arg Ser Ser Val Thr Phe Glu

	245	250	255	
	Cys Asp Leu Gly Arg Glu Val Ala Asn Glu Ala Lys Tyr Leu Cys Arg			
5	260	265	270	
	Met Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg			
	275	280	285	
10	Asp Pro Asp Phe Glu Gly Arg Ile Leu Ile Thr Pro Lys Asp Asp Asn			
	290	295	300	
	Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly			
	305	310	315	320
15	His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp			
	325	330	335	
	Pro Ile Gln Thr Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro			
20	340	345	350	
	Asn Arg Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile			
	355	360	365	
25	Ala Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys			
	370	375	380	
	Arg Trp Glu Gly Asp Gly Asn Gly His Cys Pro Ala Leu Val Gly Thr			
	385	390	395	400
30	Gln Ala Gln Val Gln Glu Glu Tyr Glu Gly Arg Leu Ala Leu Phe Asp			
	405	410	415	
	Gln Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr			
35	420	425	430	
	Glu Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Ser Arg Trp			
	435	440	445	
40	Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Arg Glu Pro Asn			
	450	455	460	
	Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Leu Gly Glu Thr Phe			
	465	470	475	480
45	Thr Val Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr			
	485	490	495	
	Trp Cys Lys Trp Ser Asn Lys Gly Cys His Ile Leu Pro Ser His Asp			
50	500	505	510	
	Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Leu			
	515	520	525	
55	Val Ser Met Thr Leu Asn Pro Val Ser Lys Glu Asp Glu Gly Trp Tyr			
	530	535	540	
	Trp Cys Gly Val Lys Gln Gly Gln Thr Tyr Gly Glu Thr Thr Ala Ile			
	545	550	555	560
60	Tyr Ile Ala Val Glu Glu Arg Thr Arg Gly Ser Ser His Val Asn Pro			
	565	570	575	
	Thr Asp Ala Asn Ala Arg Ala Lys Val Ala Leu Glu Glu Val Val			
	580	585	590	
65	Asp Ser Ser Ile Ser Glu Lys Glu Asn Lys Ala Ile Pro Asn Pro Gly			

	595	600	605
	Pro Phe Ala Asn Glu Arg Glu Ile Gln Asn Val Arg Asp Gln Ala Gln		
5	610	615	620
	Glu Asn Arg Ala Ser Gly Asp Ala Gly Ser Ala Asp Gly Gln Ser Arg		
	625	630	635
10	Ser Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu		
	645	650	655
	Val Leu Ala Val Gly Ala Ile Ala Val Trp Val Ala Arg Val Arg His		
	660	665	670
15	Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile		
	675	680	685
	Ser Met Ala Asp Phe Lys Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn		
	690	695	700
20	Met Gly Ala Ser Pro Asp Thr Gln Gln Thr Val Ile Glu Gly Lys Asp		
	705	710	715
	Glu Ile Val Thr Thr Glu Cys Thr Ala Glu Pro Glu Glu Ser Lys		
25	725	730	735
	Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala		
	740	745	750
30	Phe Leu Leu Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro		
	755	760	765
	Gln Glu Ala		
	770		
35			

(2) INFORMATION FOR SEQ ID NO: 9:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 3269 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	DESCRIPTION: Rat Polyimmunoglobulin Receptor	
	(ix) FEATURE:	
50	(A) NAME/KEY: Coding Sequence	
	(B) LOCATION: 74....2383	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
55	GGCAACGAAG GTACCATGGA TCTTATACAA GAAAGTGAACC AACATGCCGC AACCTCCTTG	60
	GAAGCCACAA GCG ATG AGG CTC TCC TTG TTC GCC CTC TTG GTA ACT GTC	109
	Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val	
	1 5 10	
60	TTC TCA GGG GTC TCC ACA CAA AGC CCC ATA TTT GGT CCC CAG GAT GTG	157
	Phe Ser Gly Val Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val	
	15 20 25	
65	AGT AGT ATT GAA GGT AAC TCG GTC TCC ATC ACG TGC TAC TAC CCA GAC	205
	Ser Ser Ile Glu Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp	

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	30	35	40	
	ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA CAA GGA GCC			253
5	Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala			
	45 50	55	60	
	AAC GGC TAC TGC GCA ACC CTC ATC TCT TCA AAT GGC TAC CTC TCG AAG			301
	Asn Gly Tyr Cys Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys			
	65	70	75	
10	GAG TAT TCA GGC AGA GCC AGC CTC ATC AAC TTC CCA GAG AAT AGC ACA			349
	Glu Tyr Ser Gly Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr			
	80	85	90	
15	TTT GTG ATT AAC ATT GCA CAT CTC ACC CAG GAG GAC ACT GGG AGC TAC			397
	Phe Val Ile Asn Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr			
	95	100	105	
20	AAG TGT GGT CTG GGT ACC ACT AAC CGA GGC CTG TTT TTC GAT GTC AGC			445
	Lys Cys Gly Leu Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser			
	110	115	120	
25	CTG GAG GTC AGC CAG GTT CCT GAG TTC CCA AAT GAC ACC CAT GTC TAC			493
	Leu Glu Val Ser Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr			
	125	130	135	140
	ACA AAG GAC ATA GGC AGA ACT GTG ACC ATC GAA TGC CGT TTC AAA GAG			541
	Thr Lys Asp Ile Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu			
	145	150	155	
30	GGG AAT GCT CAT AGC AAG AAA TCC CTG TGT AAG AAG AGA GGA GAG GCC			589
	Gly Asn Ala His Ser Lys Ser Leu Cys Lys Arg Gly Glu Ala			
	160	165	170	
35	TGC GAA GTT GTC ATC GAC TCT ACT GAG TAC GTG GAC CCC AGC TAT AAG			637
	Cys Glu Val Val Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys			
	175	180	185	
40	GAC AGA GCA ATC CTT TTT ATG AAA GGG ACC AGC CGC GAT ATA TTC TAT			685
	Asp Arg Ala Ile Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr			
	190	195	200	
45	GTC AAC ATT AGC CAC CTA ATA CCC AGT GAT GCT GGA CTG TAT GTT TGC			733
	Val Asn Ile Ser His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys			
	205	210	215	220
	CAA GCT GGA GAA GGC CCC AGT GCT GAT AAA AAT AAT GCT GAC CTC CAG			781
	Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln			
	225	230	235	
50	GTG CTA GAG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG AGG TCC TCA			829
	Val Leu Glu Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser			
	240	245	250	
55	GTG ACT TTT GAA TGT GAC CTG GGC CGT GAA GTG GCA AAT GAT GCC AAA			877
	Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys			
	255	260	265	
60	TAT CTG TGT CGG AAG AAC AAG GAA ACC TGT GAT GTC ATC ATC AAC ACC			925
	Tyr Leu Cys Arg Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr			
	270	275	280	
65	CTG GGG AAG AGA GAT CCA GCC TTT GAA GGC AGG ATC CTG CTA ACC CCC			973
	Leu Gly Lys Arg Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro			
	285	290	295	300

	AGG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC CTG AGG AAG Arg Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys 305 310 315	1021
5	GAG GAT GCA GGG CAC TAC CAG TGT GGA GCG CAC AGT TCT GGT TTG CCT Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro 320 325 330	1069
10	CAA GAA GGC TGG CCC GTC CAG GCT TGG CAA CTC TTT GTC AAT GAA GAG Gln Glu Gly Trp Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu 335 340 345	1117
15	TCC ACG ATT CCC AAT AGT CGC TCT GTT GTG AAG GGT GTC ACA GGA GGC Ser Thr Ile Pro Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly 350 355 360	1165
20	TCT GTG GCC ATC GTC TGT CCC TAT AAC CCC AAG GAA AGC AGC AGC CTC Ser Val Ala Ile Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu 365 370 375 380	1213
25	AAG TAC TGG TGT CAC TGG GAA GCC GAC GAG AAT GGA CGC TGC CCG GTG Lys Tyr Trp Cys His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val 385 390 395	1261
30	CTC GTG GGG ACC CAG GCC CTG GTG CAA GAA GGA TAT GAA GGC CGA CTG Leu Val Gly Thr Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu 400 405 410	1309
35	GCA CTG TTC GAT CAG CCG GGC AGT GGC GCC TAC ACT GTC ATC CTC AAC Ala Leu Phe Asp Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn 415 420 425	1357
40	CAG CTC ACC ACC CAG GAT TCT GGC TTC TAC TGG TGT CTT ACC GAT GGT Gln Leu Thr Thr Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly 430 435 440	1405
45	GAC TCT CGC TGG AGA ACC ACG ATA GAA CTG CAG GTT GCT GAA GCT ACA Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr 445 450 455 460	1453
50	AAG AAG CCA GAC CTT GAG GTG ACA CCA CAG AAC GCG ACC GCG GTG ATA Lys Lys Pro Asp Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile 465 470 475	1501
55	GGA GAG ACC TTC ACA ATC TCC TGC CAC TAT CCG TGC AAA TTC TAC TCC Gly Glu Thr Phe Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser 480 485 490	1549
60	CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC GAC GGC TGC CAC ATC CTG Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu 495 500 505	1597
65	CCG AGC CAT GAT GAA GGT GCC CGC CAG TCC TCT GTG AGC TGT GAC CAG Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln 510 515 520	1645
70	AGC AGC CAG ATC GTC TCC ATG ACC CTG AAC CCG GTC AAA AAG GAA GAT Ser Ser Gln Ile Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp 525 530 535 540	1693
75	GAA GGC TGG TAC TGG TGT GGG GTA AAA GAA GGT CAG GTC TAT GGA GAA Glu Gly Trp Tyr Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu 545 550 555	1741
80	ACT ACA GCC ATC TAT GTA GCA GTT GAA GAG AGG ACC AGA GGG TCA CCC Thr Thr Ala Ile Tyr Val Ala Val Glu Arg Thr Arg Gly Ser Pro	1789

	560	565	570	
5	CAC ATC AAC CCG ACA GAT GCA AAC GCA CGT GCA AAA GAT GCT CCA GAG His Ile Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu 575 580 585			1837
10	GAA GAG GCA ATG GAA TCC TCT GTC AGG GAG GAT GAA AAC AAG GCC AAT Glu Glu Ala Met Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn 590 595 600			1885
15	CTG GAC CCC AGG CTT TTT GCA GAC GAA AGA GAG ATA CAG AAT GCG GGA Leu Asp Pro Arg Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly 605 610 615 620			1933
20	GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG AAT GCT GGC AGT GCT GGT Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly 625 630 635			1981
25	GGA CAA AGC GGG AGC TCC AAA GTC CTA TTC TCC ACC CTG GTG CCC CTG Gly Gln Ser Gly Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu 640 645 650			2029
30	GGT TTG GTG CTG GCA GTG GGT GCT GTG GCT GTG TGG GTG GCC AGA GTC Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val 655 660 665			2077
35	CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC AGC AGC TAC AGG ACA Arg His Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr 670 675 680			2125
40	GAC ATT AGC ATG GGA GAC TTC AGG AAC TCC AGG GAT TTG GGA GGC AAT Asp Ile Ser Met Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn 685 690 695 700			2173
45	GAC AAC ATG GGC GCC ACT CCA GAC ACA CAA GAA ACA GTC CTC GAA GGA Asp Asn Met Gly Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly 705 710 715			2221
50	AAA GAT GAA ATA GAG ACT ACC ACC GAG TGT ACC ACC GAG CCA GAG GAA Lys Asp Glu Ile Glu Thr Thr Glu Cys Thr Glu Pro Glu Glu 720 725 730			2269
55	TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA GCT GAC ATG GCC TAC Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr 735 740 745			2317
60	TCA GCA TTC CTG TTT CAG TCC AGC ACA ATA GCT GCG CAG GTC CAT GAT Ser Ala Phe Leu Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp 750 755 760			2365
65	GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCTACCC CTGCCTGTGA CAATCAACT Gly Pro Gln Glu Ala 765			2422
70	TGAGAACATCAC ATTGATCCAC TCGCAGCCCCA CCCTCGCCCCA TCACCCAGGC TCTTCCCTCC TGTCTCAGA GGTGTGCTGG TTCCTCCCTC AGTCGTGGAA GCCTGGCCTA CTTATGCCTG TTTAGGAGAG AGCGTGAGGA GTTCTTTTG CTGTTAAAGA GTAAGGTGGA AATGAGTTGA GCCCAAGAGG TGTCTCTGAG AGACGAGGGT TCAGAGCAGG GGCTCATTTC AGGAGGAAGA GCCATTTGAA GCCTCTTAT ACACATATGC TAGGATGTCA GGATAGCTCT TCTCCTCCAT CTCTCCTTTC TTCTCTTCTT GATTCAAGACA ACAGATCCGA AAACACTCACTA GGCTTCCGGT			2482 2542 2602 2662 2722 2782

	GTCTACTAAA TGCTGAGAGT CAGGCCACAG CCTTTCTATA AACATCACTG GAAAGAGACAC	2842
	CACCTCGTCC CAGATTCTGT CTTTCCCTA AGCTATCAAT CATTACCGGG GATTCCCTT	2902
5	GCCTCTGCAC CTCATAGGCA ACAAAAGAAA CATAAGTCT GCAGTCTAAG GCATACCAA	2962
	GCCATAAGGG CACCACGAGA CTCAGATGAG AAGAGATTT TCTCCAGAGT ACTCAGTGAG	3022
10	ATAGACTAGT GTCAAGCCAG ATGGGGCAAC TCCTGGCTCT TGGCCTGGGA CTTGTCTTCA	3082
	AGATCTCTGC TCTTATTAGA GAAAGAACCT TAGCATGAG AAAAGTAAGA GAAAACAAGT	3142
	TACATGGGCA TGGTGGTGTG CTCCGTCAAT CCCAATATTA AGAGGTTAAA AAATAGGACC	3202
15	AGAAGTTAA AGTAATCCTT GGCTACCTAG TGAGTGTAAAG GCCAGCCTGG AATCAATAAG	3262
	AGTTGGT	3269

20 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH:	770 amino acids
	(B) TYPE:	amino acid
	(C) STRANNESS:	single
	(D) TOPOLOGY:	linear
	DESCRIPTION:	Rat Polyimmunoglobulin Receptor

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val Phe Ser Gly Val				
1	5	10	15	
Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val Ser Ser Ile Glu				
35	20	25	30	
Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn				
40	35	40	45	
Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Asn Gly Tyr Cys				
50	55	60		
Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly				
45	65	70	75	80
Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr Phe Val Ile Asn				
85	90	95		
Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr Lys Cys Gly Leu				
50	100	105	110	
Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser Leu Glu Val Ser				
55	115	120	125	
Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr Thr Lys Asp Ile				
130	135	140		
60	Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu Gly Asn Ala His			
145	150	155	160	
Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala Cys Glu Val Val				
165	170	175		
65	Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys Asp Arg Ala Ile			

	180	185	190
	Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr Val Asn Ile Ser		
5	195 200	205	
	His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys Gln Ala Gly Glu		
	210 215	220	
10	Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln Val Leu Glu Pro		
	225 230	235	240
	Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu		
	245 250	255	
15	Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys Tyr Leu Cys Arg		
	260 265	270	
20	Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg		
	275 280	285	
	Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro Arg Asp Asp Asn		
	290 295	300	
25	Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly		
	305 310	315	320
	His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp		
	325 330	335	
30	Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro		
	340 345	350	
35	Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile		
	355 360	365	
	Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys		
	370 375	380	
40	His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val Leu Val Gly Thr		
	385 390	395	400
	Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu Ala Leu Phe Asp		
	405 410	415	
45	Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr		
	420 425	430	
50	Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly Asp Ser Arg Trp		
	435 440	445	
	Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Lys Lys Pro Asp		
	450 455	460	
55	Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile Gly Glu Thr Phe		
	465 470	475	480
	Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr		
	485 490	495	
60	Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu Pro Ser His Asp		
	500 505	510	
65	Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Ile		
	515 520	525	

Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp Glu Gly Trp Tyr
 530 535 540

5 Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu Thr Thr Ala Ile
 545 550 555 560

Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro His Ile Asn Pro
 565 570 575

10 Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu Glu Ala Met
 580 585 590

Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn Leu Asp Pro Arg
 595 600 605

15 Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly Asp Gln Ala Gln
 610 615 620

Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly Gly Gln Ser Gly
 625 630 635 640

Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu Val Leu
 645 650 655

25 Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val Arg His Arg Lys
 660 665 670

Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile Ser Met
 675 680 685

30 Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn Met Gly
 690 695 700

Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly Lys Asp Glu Ile
 705 710 715 720

Glu Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu Ser Lys Lys Ala
 725 730 735

40 Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala Phe Leu
 740 745 750

Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro Gln Glu
 755 760 765

45 Ala

50 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
 55 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Kappa

60 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 8....320

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTCGAGC GAC ATT GTG ATG ACC CAG TCT CCA GCA ATC ATG TCT GCA TCT Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser 1 5 10	49
5 CCA GGG GAG AAG GTC ACC ATA ACC TGC AGT GCC AGC TCA AGT GTA AGT Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Val Ser 15 20 25 30	97
10 TAC ATG CAC TGG TTC CAG CAG AAG CCA GGC ACT TCT CCC AAA CTC TGG Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp 35 40 45	145
15 CTT TAT AGC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser 50 55 60	193
20 GGC AGT GGA TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC CGA ATG GAG Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu 65 70 75	241
25 GCT GAA GAT GCT GCC ACT TAT TAC TGC CAT CAA AGG ACT AGT TAC CCG Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro 80 85 90	289
30 (2) INFORMATION FOR SEQ ID NO: 12: (i) SEQUENCE CHARACTERISTICS: 35 (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDENESS: single (D) TOPOLOGY: linear DESCRIPTION: Guy's 13 Kappa	322
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly 1 5 10 15	
45 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 20 25 30	
50 His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Leu Tyr 35 40 45	
55 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser 50 55 60	
60 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu 65 70 75 80	
65 Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro Tyr Thr 85 90 95	
60 Phe Gly Gly Gly Thr Lys Leu Glu Ile 100 105	
65 (2) INFORMATION FOR SEQ ID NO: 13:	

(i) SEQUENCE CHARACTERISTICS:

10 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 7...402

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CTCGAG ATG GAA TGG ACC TGG GTT TTT CTC TTC CTC CTG TCA GGA ACT Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr	1 5 10	48
GCA GGC GTC CAC TCT GGG GTC CAG CTT CAG CAG TCA GGA CCT GAC CTG Ala Gly Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu	15 20 25 30	96
GTG AAA CCT GGG GCC TCA GTG AAG ATA TCC TGC AAG GCT TCT GGA TAC Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr	35 40 45	144
ACA TTC ACT GAC TAC AAC ATA CAC TGG GTG AAG CAG AGC CGT GGA AAG Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys	50 55 60	192
AGC CTT GAG TGG ATT GGA TAT ATT TAT CCT TAC AAT GGT AAT ACT TAC Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr	65 70 75	240
TAC AAC CAG AAG TTC AAG AAC AAG GCC ACA TTG ACT GTA GAC AAT TCC Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser	80 85 90	288
TCC ACC TCA GCC TAC ATG GAG CTC CGC AGC CTG ACA TCT GAG GAC TCT Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser	95 100 105 110	336
GCA GTC TAT TAC TGT GCA ACC TAC TTT GAC TAC TGG GGC CAA GGC ACC Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr	115 120 125	384
ACT CTC ACA GTC TCC TCA Thr Leu Thr Val Ser Ser	130	402

55 (2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15

5 Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

10 Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu
 50 55 60

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn
 65 70 75 80

15 Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr
 85 90 95

20 Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
 115 120 125

25 Thr Val Ser Ser
 130

30

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACCAGATCTA TGGAATGGAC CTGGGTTTT C 31

45

50 (2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

65 CCCAAGCTTG GTTTTGGAGA TGGTTTCCTC 30

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17.

- GATAAGCTTG GTCCTACTCC TCCTGCTCCT A

31

15 (2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AATCTCGAGT CAGTAGCAGA TGCCATCTCC

30

30

35 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGAAAGCTTT GTACATATGC AAGGCTTACA

30